

# SEQUENCE LISTING

<110> Nissan Chemical Industries, Ltd.

Center for Advanced Science and Technology Incubation, Ltd.

<120> Adiponectin receptors and genes coding the same

<160> 8

<210> 1

<211> 1128

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (1125)

<400> 1

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Met Ser Ser His Lys Gly Ser Val Val Ala Gln Gly Asn Gly Ala Pro

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gcc agt aac agg gaa gct gac acg gtg gaa ctg gct gaa ctg gga ccc 96

Ala Ser Asn Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro

20 25 30

ctg cta gaa gag aag ggc aaa cgg gta atc gcc aac cca ccc aaa gct 144

Leu Leu Glu Glu Lys Gly Lys Arg Val Ile Ala Asn Pro Pro Lys Ala

35	40	45	
gaa gaa gag caa aca tgc cca gtg ccc cag gaa gaa gag gag gag gtg			192
Glu Glu Glu Gln Thr Cys Pro Val Pro Gln Glu Glu Glu Glu Glu Val			
50	55	60	
cgg gta ctg aca ctt ccc ctg caa gcc cac cac gcc atg gag aag atg			240
Arg Val Leu Thr Leu Pro Leu Gln Ala His His Ala Met Glu Lys Met			
65	70	75	80
gaa gag ttt gtg tac aag gtc tgg gag gga cgt tgg agg gtc atc cca			288
Glu Glu Phe Val Tyr Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro			
	85	90	95
tat gat gtg ctc cct gac tgg cta aag gac aac gac tat ctg cta cat			336
Tyr Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp Tyr Leu Leu His			
100	105	110	
ggt cat aga cct ccc atg ccc tcc ttt cgg gct tgc ttc aag agc atc			384
Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile			
115	120	125	
ttc cgc att cat aca gaa act ggc aac atc tgg acc cat ctg ctt ggt			432
Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly			
130	135	140	
ttc gtg ctg ttt ctc ttt ttg gga atc ttg acc atg ctc aga cca aat			480
Phe Val Leu Phe Leu Phe Leu Gly Ile Leu Thr Met Leu Arg Pro Asn			
145	150	155	160

atg tac ttc atg gcc cct cta cag gag aag gtg gtt ttt ggg atg ttc	528
Met Tyr Phe Met Ala Pro Leu Gln Glu Lys Val Val Phe Gly Met Phe	
165 170 175	
ttt ttg ggt gca gtg ctc tgc ctc agc ttc tcc tgg ctc ttt cac acc	576
Phe Leu Gly Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr	
180 185 190	
gtc tat tgt cat tca gag aaa gtc tct cgg act ttt tcc aaa ctg gac	624
Val Tyr Cys His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp	
195 200 205	
tat tca ggg att gct ctt cta att atg ggg agc ttt gtc ccc tgg ctc	672
Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu	
210 215 220	
tat tat tcc ttc tac tgc tcc cca cag cca cgg ctc atc tac ctc tcc	720
Tyr Tyr Ser Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser	
225 230 235 240	
atc gtc tgt gtc ctg ggc att tct gcc atc att gtg gcg cag tgg gac	768
Ile Val Cys Val Leu Gly Ile Ser Ala Ile Ile Val Ala Gln Trp Asp	
245 250 255	
cgg ttt gcc act cct aag cac cgg cag aca aga gca ggc gtg ttc ctg	816
Arg Phe Ala Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu	
260 265 270	

gga ctt ggc ttg agt ggc gtc gtg ccc acc atg cac ttt act atc gct	864
Gly Leu Gly Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala	
275 280 285	
gag ggc ttt gtc aag gcc acc aca gtg ggc cag atg ggc tgg ttc ttc	912
Glu Gly Phe Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe	
290 295 300	
ctc atg gct gtg atg tac atc act gga gct ggc ctt tat gct gct cga	960
Leu Met Ala Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg	
305 310 315 320	
att cct gag cgc ttc ttt cct gga aaa ttt gac ata tgg ttc cag tct	1008
Ile Pro Glu Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser	
325 330 335	
cat cag att ttc cat gtc ctg gtg gtg gca gca gcc ttt gtc cac ttc	1056
His Gln Ile Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe	
340 345 350	
tat gga gtc tcc aac ctt cag gaa ttc cgt tac ggc cta gaa ggc ggc	1104
Tyr Gly Val Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly	
355 360 365	
tgt act gat gac acc ctt ctc tga	1128
Cys Thr Asp Asp Thr Leu Leu	
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<210> 2

<211> 375

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Ser His Lys Gly Ser Val Val Ala Gln Gly Asn Gly Ala Pro

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Ala Ser Asn Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro

20 25 30

Leu Leu Glu Glu Lys Gly Lys Arg Val Ile Ala Asn Pro Pro Lys Ala

35 40 45

Glu Glu Glu Gln Thr Cys Pro Val Pro Gln Glu Glu Glu Glu Val

50 55 60

Arg Val Leu Thr Leu Pro Leu Gln Ala His His Ala Met Glu Lys Met

65 70 75 80

Glu Glu Phe Val Tyr Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro

85 90 95

Tyr Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp Tyr Leu Leu His

100 105 110

Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile

115 120 125

Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly  
130 135 140

Phe Val Leu Phe Leu Phe Leu Gly Ile Leu Thr Met Leu Arg Pro Asn  
145 150 155 160

Met Tyr Phe Met Ala Pro Leu Gln Glu Lys Val Val Phe Gly Met Phe  
165 170 175

Phe Leu Gly Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr  
180 185 190

Val Tyr Cys His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp  
195 200 205

Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu  
210 215 220

Tyr Tyr Ser Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser  
225 230 235 240

Ile Val Cys Val Leu Gly Ile Ser Ala Ile Ile Val Ala Gln Trp Asp  
245 250 255

Arg Phe Ala Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu  
260 265 270

Gly Leu Gly Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala

275	280	285
Glu Gly Phe Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe		
290	295	300
Leu Met Ala Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg		
305	310	315 320
Ile Pro Glu Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser		
325	330	335
His Gln Ile Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe		
340	345	350
Tyr Gly Val Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly		
355	360	365
Cys Thr Asp Asp Thr Leu Leu		
370	375	

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<211> 900

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<213> Homo sapiens

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<221> CDS

<222> (1).. (897)

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cga gtg atc cct cat gat gta cta cca gac tgg ctc aag gat aat gac	96
Arg Val Ile Pro His Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp	
20 25 30	
ttc ctc ttg cat gga cac cgg cct cct atg cct tct ttc cgg gcc tgt	144
Phe Leu Leu His Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys	
35 40 45	
ttt aag agc att ttc aga ata cac aca gaa aca ggc aac att tgg aca	192
Phe Lys Ser Ile Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr	
50 55 60	
cat ctc tta ggt tgt gta ttc ttc ctg tgc ctg ggg atc ttt tat atg	240
His Leu Leu Gly Cys Val Phe Phe Leu Cys Leu Gly Ile Phe Tyr Met	
65 70 75 80	
ttt cgc cca aat atc tcc ttt gtg gcc cct ctg caa gag aag gtg gtc	288
Phe Arg Pro Asn Ile Ser Phe Val Ala Pro Leu Gln Glu Lys Val Val	
85 90 95	
ttt gga tta ttt ttc tta gga gcc att ctc tgc ctt tct ttt tca tgg	336
Phe Gly Leu Phe Phe Leu Gly Ala Ile Leu Cys Leu Ser Phe Ser Trp	



100	105	110	
ctc ttc cac aca gtc tac tgc cac tca gag ggg gtc tct cgg ctc ttc			384
Leu Phe His Thr Val Tyr Cys His Ser Glu Gly Val Ser Arg Leu Phe			
115	120	125	
tct aaa ctg gat tac tct ggt att gct ctt ctg att atg gga agt ttt			432
Ser Lys Leu Asp Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe			
130	135	140	
gtt cct tgg ctt tat tat tct ttc tac tgt aat cca caa cct tgc ttc			480
Val Pro Trp Leu Tyr Tyr Ser Phe Tyr Cys Asn Pro Gln Pro Cys Phe			
145	150	155	160
atc tac ttg att gtc atc tgt gtg ctg ggc att gca gcc att ata gtc			528
Ile Tyr Leu Ile Val Ile Cys Val Leu Gly Ile Ala Ala Ile Ile Val			
165	170	175	
tcc cag tgg gac atg ttt gcc acc cct cag tat cgg gga gta aga gca			576
Ser Gln Trp Asp Met Phe Ala Thr Pro Gln Tyr Arg Gly Val Arg Ala			
180	185	190	
gga gtg ttt ttg ggc cta ggc ctg agt gga atc att cct acc ttg cac			624
Gly Val Phe Leu Gly Leu Gly Leu Ser Gly Ile Ile Pro Thr Leu His			
195	200	205	
tat gtc atc tcg gag ggg ttc ctt aag gcc gcc acc ata ggg cag ata			672
Tyr Val Ile Ser Glu Gly Phe Leu Lys Ala Ala Thr Ile Gly Gln Ile			
210	215	220	

ggc tgg ttg atg ctg atg gcc agc ctc tac atc aca gga gct gcc ctg 720  
 Gly Trp Leu Met Leu Met Ala Ser Leu Tyr Ile Thr Gly Ala Ala Leu  
 225 230 235 240

tat gct gcc cgg atc ccc gaa cgc ttt ttc cct ggc aaa tgt gac atc 768  
 Tyr Ala Ala Arg Ile Pro Glu Arg Phe Phe Pro Gly Lys Cys Asp Ile  
 245 250 255

tgg ttt cac tct cat cag ctg ttt cat atc ttt gtg gtt gct gga gct 816  
 Trp Phe His Ser His Gln Leu Phe His Ile Phe Val Val Ala Gly Ala  
 260 265 270

ttt gtt cac ttc cat ggt gtc tca aac ctc cag gag ttt cgt ttc atg 864  
 Phe Val His Phe His Gly Val Ser Asn Leu Gln Glu Phe Arg Phe Met  
 275 280 285

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<210> 4

<211> 299

<212> PRT

<213> Homo sapiens

<400> 4

Met Glu Lys Met Glu Glu Phe Val Cys Lys Val Trp Glu Gly Arg Trp

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Arg Val Ile Pro His Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp			
20	25	30	
Phe Leu Leu His Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys			
35	40	45	
Phe Lys Ser Ile Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr			
50	55	60	
His Leu Leu Gly Cys Val Phe Phe Leu Cys Leu Gly Ile Phe Tyr Met			
65	70	75	80
Phe Arg Pro Asn Ile Ser Phe Val Ala Pro Leu Gln Glu Lys Val Val			
85	90	95	
Phe Gly Leu Phe Phe Leu Gly Ala Ile Leu Cys Leu Ser Phe Ser Trp			
100	105	110	
Leu Phe His Thr Val Tyr Cys His Ser Glu Gly Val Ser Arg Leu Phe			
115	120	125	
Ser Lys Leu Asp Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe			
130	135	140	
Val Pro Trp Leu Tyr Tyr Ser Phe Tyr Cys Asn Pro Gln Pro Cys Phe			
145	150	155	160

Ile Tyr Leu Ile Val Ile Cys Val Leu Gly Ile Ala Ala Ile Ile Val  
165 170 175

Ser Gln Trp Asp Met Phe Ala Thr Pro Gln Tyr Arg Gly Val Arg Ala  
180 185 190

Gly Val Phe Leu Gly Leu Gly Leu Ser Gly Ile Ile Pro Thr Leu His  
195 200 205

Tyr Val Ile Ser Glu Gly Phe Leu Lys Ala Ala Thr Ile Gly Gln Ile  
210 215 220

Gly Trp Leu Met Leu Met Ala Ser Leu Tyr Ile Thr Gly Ala Ala Leu  
225 230 235 240

Tyr Ala Ala Arg Ile Pro Glu Arg Phe Phe Pro Gly Lys Cys Asp Ile  
245 250 255

Trp Phe His Ser His Gln Leu Phe His Ile Phe Val Val Ala Gly Ala  
260 265 270

Phe Val His Phe His Gly Val Ser Asn Leu Gln Glu Phe Arg Phe Met  
275 280 285

Ile Gly Gly Gly Cys Ser Glu Glu Asp Ala Leu  
290 295

<210> 5

<211> 1128

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1125)

<400> 5

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15

tct ggt aac aga gaa gct gac aca gtg gag ctg gct gag ctg ggg ccc 96

Ser Gly Asn Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro

20

25

30

ctg ctg gag gag aag ggc aag cgg gca gcc agc agc cca gcc aag gct 144

Leu Leu Glu Glu Lys Gly Lys Arg Ala Ala Ser Ser Pro Ala Lys Ala

35

40

45

gag gaa gat caa gca tgc ccg gtg cct cag gaa gag gag gag gag gtg 192

Glu Glu Asp Gln Ala Cys Pro Val Pro Gln Glu Glu Glu Glu Glu Val

50

55

60

cgg gtg ctg acg ctt cct ctg caa gcc cac cat gcc atg gag aag atg 240

Arg Val Leu Thr Leu Pro Leu Gln Ala His His Ala Met Glu Lys Met

65

70

75

80

gag gag ttc gtg tat aag gtc tgg gag gga cgt tgg aga gtc atc ccg	288
Glu Glu Phe Val Tyr Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro	
85 90 95	
tat gat gtg ctt cct gac tgg ctg aaa gac aac gac tac ctg cta cat	336
Tyr Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp Tyr Leu Leu His	
100 105 110	
ggc cac aga cca cct atg ccc tcc ttt cgg gct tgc ttc aag agc atc	384
Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile	
115 120 125	
ttc cgc atc cac aca gag act ggc aac atc tgg aca cat ctg ctt ggt	432
Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly	
130 135 140	
ttt gtg cta ttt ctc ttt ctg gga atc ttg acg atg ctg aga cca aat	480
Phe Val Leu Phe Leu Phe Leu Gly Ile Leu Thr Met Leu Arg Pro Asn	
145 150 155 160	
atg tac ttc atg gct ccc ctg cag gag aag gtg gtc ttc ggg atg ttc	528
Met Tyr Phe Met Ala Pro Leu Gln Glu Lys Val Val Phe Gly Met Phe	
165 170 175	
ttc ctg ggc gcg gtg ctc tgc ctc agt ttc tcc tgg ctc ttc cac act	576
Phe Leu Gly Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr	
180 185 190	
gtc tac tgt cat tca gag aag gtc tct cgg act ttt tcc aaa ctg gac	624

Val Tyr Cys His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp  
195 200 205

tat tca ggg att gct cta ctg att atg ggg agc ttc gtt ccc tgg ctc 672  
Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu  
210 215 220

tat tac tcc ttc tac tgc tcc cca cag ccg cgg ctc atc tac ctc tcc 720  
Tyr Tyr Ser Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser  
225 230 235 240

atc gtc tgt gtc ctg ggc atc tct gcc atc att gtg gca cag tgg gac 768  
Ile Val Cys Val Leu Gly Ile Ser Ala Ile Ile Val Ala Gln Trp Asp  
245 250 255

cgg ttt gcc act ccc aag cac cgg cag aca aga gca gga gtg ttc ctg 816  
Arg Phe Ala Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu  
260 265 270

gga ctt ggc ttg agt ggt gtt gta ccc acc atg cac ttt act atc gct 864  
Gly Leu Gly Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala  
275 280 285

gag ggc ttt gtc aag gcc acc acg gtg ggc cag atg ggc tgg ttc ttc 912  
Glu Gly Phe Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe  
290 295 300

ctc atg gct gtg atg tac atc acc ggc gcc ggc ctg tat gct gct cgg 960  
Leu Met Ala Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg

305	310	315	320	
att cct gag cgc ttc ttc cct gga aaa ttt gac atc tgg ttc cag tct				1008
Ile Pro Glu Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser				
	325	330	335	
cat cag att ttc cac gtc ctg gtg gtg gca gca gct ttc gtc cac ttc				1056
His Gln Ile Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe				
	340	345	350	
tat ggt gtg tcc aac ctt cag gaa ttc cgt tat ggc cta gaa ggt ggc				1104
Tyr Gly Val Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly				
	355	360	365	
tgt acc gac gac tcc ctt ctc tga				1128
Cys Thr Asp Asp Ser Leu Leu				
	370	375		

<210> 6

<211> 375

<212> PRT

<213> Mus musculus

<400> 6

Met Ser Ser His Lys Gly Ser Ala Gly Ala Gln Gly Asn Gly Ala Pro

1	5	10	15
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Ser Gly Asn Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro



	20		25		30
Leu	Leu	Glu	Glu	Lys	Gly
				Lys	Arg
				Ala	Ala
				Ser	Ser
				Pro	Ala
				Lys	Ala
	35		40		45
Glu	Glu	Asp	Gln	Ala	Cys
				Pro	Val
				Pro	Gln
				Glu	Glu
				Glu	Glu
				Glu	Glu
	50		55		60
Arg	Val	Leu	Thr	Leu	Pro
				Leu	Gln
				Ala	His
				His	Ala
				Met	Glu
				Lys	Met
	65		70		75
Glu	Glu	Phe	Val	Tyr	Lys
				Val	Trp
				Glu	Gly
				Arg	Trp
				Arg	Val
				Ile	Pro
		85		90	95
Tyr	Asp	Val	Leu	Pro	Asp
				Trp	Leu
				Lys	Asp
				Asn	Asp
				Tyr	Leu
				Leu	His
	100		105		110
Gly	His	Arg	Pro	Pro	Met
				Pro	Ser
				Phe	Arg
				Ala	Cys
				Phe	Lys
				Ser	Ile
	115		120		125
Phe	Arg	Ile	His	Thr	Glu
				Thr	Gly
				Asn	Ile
				Trp	Thr
				His	Leu
				Leu	Gly
	130		135		140
Phe	Val	Leu	Phe	Leu	Phe
				Leu	Gly
				Ile	Leu
				Thr	Met
				Leu	Arg
				Pro	Asn
	145		150		155
Met	Tyr	Phe	Met	Ala	Pro
				Leu	Gln
				Glu	Lys
				Val	Val
				Phe	Gly
				Met	Phe
	165		170		175

Phe Leu Gly Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr  
180 185 190

Val Tyr Cys His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp  
195 200 205

Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu  
210 215 220

Tyr Tyr Ser Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser  
225 230 235 240

Ile Val Cys Val Leu Gly Ile Ser Ala Ile Ile Val Ala Gln Trp Asp  
245 250 255

Arg Phe Ala Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu  
260 265 270

Gly Leu Gly Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala  
275 280 285

Glu Gly Phe Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe  
290 295 300

Leu Met Ala Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg  
305 310 315 320

Ile Pro Glu Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser  
325 330 335

His Gln Ile Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe

340

345

350

Tyr Gly Val Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly

355

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365

Cys Thr Asp Asp Ser Leu Leu

370

375

<210> 7

<211> 936

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1).. (933)

<400> 7

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Met Gly Met Ser Pro Leu Leu Gln Ala His His Ala Met Glu Arg Met

1

5

10

15

gaa gag ttt gtt tgt aag gtg tgg gaa ggc cga tgg cga gtg atc cct 96

Glu Glu Phe Val Cys Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro

20

25

30

cac gat gtg cta ccg gat tgg ctt aag gat aat gac ttc ctt ctc cat 144  
 His Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp Phe Leu Leu His

35

40

45

gga cac cgg cct cct atg cct tcc ttt cgg gcc tgt ttt aag agc att 192  
 Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile

50

55

60

ttt aga ata cac aca gag acg ggc aac att tgg aca cat ctc cta ggt 240  
 Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly

65

70

75

80

tgt gta ttc ttc ctg tgc ctg ggg atc ttt tat atg ttt cgc cca aat 288  
 Cys Val Phe Phe Leu Cys Leu Gly Ile Phe Tyr Met Phe Arg Pro Asn

85

90

95

ata tct ttt gtg gcc cct ctg caa gag aaa gtg gtc ttt ggc ttg ttc 336  
 Ile Ser Phe Val Ala Pro Leu Gln Glu Lys Val Val Phe Gly Leu Phe

100

105

110

ttc ttg gga gcc att ctc tgc ctt tcc ttt tca tgg ctc ttc cac acg 384  
 Phe Leu Gly Ala Ile Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr

115

120

125

gtg tac tgc cac tca gaa ggg gtc tcc cga ctc ttc tct aaa ttg gat 432  
 Val Tyr Cys His Ser Glu Gly Val Ser Arg Leu Phe Ser Lys Leu Asp

130

135

140

tac tct ggt att gct ctt ctg atc atg gga agt ttt gtt cct tgg ctt 480

Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu	
145	150 155 160
tat tat tct ttc tac tgt aac cca caa cct tgc ttc atc tac ctg att	528
Tyr Tyr Ser Phe Tyr Cys Asn Pro Gln Pro Cys Phe Ile Tyr Leu Ile	
165	170 175
gtc atc tgt gtg ctg ggc att gca gcc att atc gtc tct cag tgg gac	576
Val Ile Cys Val Leu Gly Ile Ala Ala Ile Ile Val Ser Gln Trp Asp	
180	185 190
atg ttt gcc acc cct cag tat cgg ggg gtc aga gca gga gtg ttc gtg	624
Met Phe Ala Thr Pro Gln Tyr Arg Gly Val Arg Ala Gly Val Phe Val	
195	200 205
ggc tta ggc ctg agt gga atc atc cct acc ttg cat tat gtc atc tca	672
Gly Leu Gly Leu Ser Gly Ile Ile Pro Thr Leu His Tyr Val Ile Ser	
210	215 220
gaa ggg ttc ctg aag gct gcc acc ata ggg cag ata ggc tgg cta atg	720
Glu Gly Phe Leu Lys Ala Ala Thr Ile Gly Gln Ile Gly Trp Leu Met	
225	230 235 240
ctt atg gct agc ctc tat atc acc gga gct gcc ctc tat gcg gcc cgt	768
Leu Met Ala Ser Leu Tyr Ile Thr Gly Ala Ala Leu Tyr Ala Ala Arg	
245	250 255
atc cct gag cgc ttc ttt cct ggc aaa tgt gac atc tgg ttt cac tct	816
Ile Pro Glu Arg Phe Phe Pro Gly Lys Cys Asp Ile Trp Phe His Ser	

260 265 270

cat cag ctc ttc cac atc ttt gtg gtt gct ggt gcc ttt gtt cac ttc 864

His Gln Leu Phe His Ile Phe Val Val Ala Gly Ala Phe Val His Phe

275 280 285

cac gga gtc tca aac ctg cag gaa ttt cgt ttc atg att ggc ggg ggc 912  
 His Gly Val Ser Asn Leu Gln Glu Phe Arg Phe Met Ile Gly Gly Gly  
 290 295 300

tgc act gaa gag gat gca ctg tga 936  
Cys Thr Glu Glu Asp Ala Leu  
305 310

&lt;210&gt; 8

<211> 311

&lt;212&gt; PRT

<213> Mus musculus

<400> 8

Met Gly Met Ser Pro Leu Leu Gln Ala His His Ala Met Glu Arg Met  
1 5 10 15

Glu Glu Phe Val Cys Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro  
20 25 30

His Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp Phe Leu Leu His  
35 40 45

Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile

50

55

60

Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly

65

70

75

80

Cys Val Phe Phe Leu Cys Leu Gly Ile Phe Tyr Met Phe Arg Pro Asn

85

90

95

Ile Ser Phe Val Ala Pro Leu Gln Glu Lys Val Val Phe Gly Leu Phe

100

105

110

Phe Leu Gly Ala Ile Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr

115

120

125

Val Tyr Cys His Ser Glu Gly Val Ser Arg Leu Phe Ser Lys Leu Asp

130

135

140

Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu

145

150

155

160

Tyr Tyr Ser Phe Tyr Cys Asn Pro Gln Pro Cys Phe Ile Tyr Leu Ile

165

170

175

Val Ile Cys Val Leu Gly Ile Ala Ala Ile Ile Val Ser Gln Trp Asp

180

185

190

Met Phe Ala Thr Pro Gln Tyr Arg Gly Val Arg Ala Gly Val Phe Val

195	200	205
Gly Leu Gly Leu Ser Gly Ile Ile Pro Thr Leu His Tyr Val Ile Ser		
210	215	220
Glu Gly Phe Leu Lys Ala Ala Thr Ile Gly Gln Ile Gly Trp Leu Met		
225	230	235 240
Leu Met Ala Ser Leu Tyr Ile Thr Gly Ala Ala Leu Tyr Ala Ala Arg		
	245	250 255
Ile Pro Glu Arg Phe Phe Pro Gly Lys Cys Asp Ile Trp Phe His Ser		
260	265	270
His Gln Leu Phe His Ile Phe Val Val Ala Gly Ala Phe Val His Phe		
275	280	285
His Gly Val Ser Asn Leu Gln Glu Phe Arg Phe Met Ile Gly Gly Gly		
290	295	300
Cys Thr Glu Glu Asp Ala Leu		
305	310	